

RAW SEQUENCE LISTING

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Application Serial Number: 10/817,530A
Source: IFWJ
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/817,530A

DATE: 11/08/2004
TIME: 16:24:16

Input Set : A:\Supp.Sequence List for.10817530.txt
Output Set: N:\CRF4\11082004\J817530A.raw

3 <110> APPLICANT: Braun, Werner
 4 Mathura, Venkatarajan S.
 5 Schein, Catherine H.
 7 <120> TITLE OF INVENTION: PHYSICAL-CHEMICAL PROPERTY BASED SEQUENCE MOTIFS AND METHODS
 8 REGARDING SAME
 10 <130> FILE REFERENCE: 265.00400101
 12 <140> CURRENT APPLICATION NUMBER: 10/817,530A
 13 <141> CURRENT FILING DATE: 2004-04-02
 15 <150> PRIOR APPLICATION NUMBER: US 60/460,769
 16 <151> PRIOR FILING DATE: 2003-04-04
 18 <160> NUMBER OF SEQ ID NOS: 5
 20 <170> SOFTWARE: PatentIn version 3.2
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 10
 24 <212> TYPE: PRT
 25 <213> ORGANISM: ARTIFICIAL SEQUENCE
 27 <220> FEATURE:
 28 <223> OTHER INFORMATION: MEMBER OF DNase-I SUPERFAMILY
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 33 1 5 10
 36 <210> SEQ ID NO: 2
 37 <211> LENGTH: 275
 38 <212> TYPE: PRT
 39 <213> ORGANISM: ARTIFICIAL SEQUENCE
 41 <220> FEATURE:
 42 <223> OTHER INFORMATION: MEMBER OF DNase-I SUPERFAMILY
 44 <400> SEQUENCE: 2
 46 Leu Tyr Glu Asp Pro Pro Asp Gln Lys Thr Ser Pro Ser Gly Lys Pro
 47 1 5 10 15
 50 Ala Thr Leu Lys Ile Cys Ser Trp Asn Val Asp Gly Leu Arg Ala Trp
 51 20 25 30
 54 Ile Lys Lys Gly Leu Asp Trp Val Lys Glu Glu Ala Pro Asp Ile
 55 35 40 45
 58 Leu Cys Leu Gln Glu Thr Lys Cys Ser Glu Asn Lys Leu Pro Ala Glu
 59 50 55 60
 62 Leu Gln Glu Leu Pro Gly Leu Ser His Gln Tyr Trp Ser Ala Pro Ser
 63 65 70 75 80
 66 Asp Lys Glu Gly Tyr Ser Gly Val Gly Leu Leu Ser Arg Gln Cys Pro
 67 85 90 95
 70 Leu Lys Val Ser Tyr Gly Ile Gly Asp Glu Glu His Asp Gln Glu Gly
 71 100 105 110
 74 Arg Val Ile Val Ala Glu Phe Asp Ser Phe Val Leu Val Thr Ala Tyr

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75	115	120	125	
78	Val Pro Asn Ala Gly Arg Gly Leu Val Arg Leu Glu Tyr Arg Gln Arg			
79	130	135	140	
82	Trp Asp Glu Ala Phe Arg Lys Phe Leu Lys Gly Leu Ala Ser Arg Lys			
83	145	150	155	160
86	Pro Leu Val Leu Cys Gly Asp Leu Asn Val Ala His Glu Glu Ile Asp			
87	165	170	175	
90	Leu Arg Asn Pro Lys Gly Asn Lys Lys Asn Ala Gly Phe Thr Pro Gln			
91	180	185	190	
94	Glu Arg Gln Gly Phe Gly Glu Leu Leu Gln Ala Val Pro Leu Ala Asp			
95	195	200	205	
98	Ser Phe Arg His Leu Tyr Pro Asn Thr Pro Tyr Ala Tyr Thr Phe Trp			
99	210	215	220	
102	Thr Tyr Met Met Asn Ala Arg Ser Lys Asn Val Gly Trp Arg Leu Asp			
103	225	230	235	240
106	Tyr Phe Leu Leu Ser His Ser Leu Leu Pro Ala Leu Cys Asp Ser Lys			
107	245	250	255	
110	Ile Arg Ser Lys Ala Leu Gly Ser Asp His Cys Pro Ile Thr Leu Tyr			
111	260	265	270	
114	Leu Ala Leu			
115	275			
118	<210> SEQ ID NO: 3			
119	<211> LENGTH: 268			
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128	Met Lys Phe Val Ser Phe Asn Ile Asn Gly Leu Arg Ala Arg Pro His			
129	1	5	10	15
132	Gln Leu Glu Ala Ile Val Glu Lys His Gln Pro Asp Val Ile Gly Leu			
133	20	25	30	
136	Gln Glu Thr Lys Val His Asp Asp Met Phe Pro Leu Glu Glu Val Ala			
137	35	40	45	
140	Lys Leu Gly Tyr Asn Val Phe Tyr His Gly Gln Lys Gly His Tyr Gly			
141	50	55	60	
144	Val Ala Leu Leu Thr Lys Glu Thr Pro Ile Ala Val Arg Arg Gly Phe			
145	65	70	75	80
148	Pro Gly Asp Asp Glu Glu Ala Gln Arg Arg Ile Ile Met Ala Glu Ile			
149	85	90	95	
152	Pro Ser Leu Leu Gly Asn Val Thr Val Ile Asn Gly Tyr Phe Pro Gln			
153	100	105	110	
156	Gly Glu Ser Arg Asp His Pro Ile Lys Phe Pro Ala Lys Ala Gln Phe			
157	115	120	125	
160	Tyr Gln Asn Leu Gln Asn Tyr Leu Glu Thr Glu Leu Lys Arg Asp Asn			
161	130	135	140	
164	Pro Val Leu Ile Met Gly Asp Met Asn Ile Ser Pro Thr Asp Leu Asp			
165	145	150	155	160
168	Ile Gly Ile Gly Glu Glu Asn Arg Lys Arg Trp Leu Arg Thr Gly Lys			

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169	165	170	175
172	Cys Ser Phe Leu Pro Glu Glu Arg Glu Trp Met Asp Arg Leu Met Ser		
173	180	185	190
176	Trp Gly Leu Val Asp Thr Phe Arg His Ala Asn Pro Gln Thr Ala Asp		
177	195	200	205
180	Arg Phe Ser Trp Phe Asp Tyr Arg Ser Lys Gly Phe Asp Asp Asn Arg		
181	210	215	220
184	Gly Leu Arg Ile Asp Leu Leu Ala Ser Gln Pro Leu Ala Glu Cys		
185	225	230	235
188	Cys Val Glu Thr Gly Ile Asp Tyr Glu Ile Arg Ser Met Glu Lys Pro		
189	245	250	255
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193	260	265	
196	<210> SEQ ID NO: 4		
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204	<400> SEQUENCE: 4		
206	Leu Lys Ile Ala Ala Phe Asn Ile Arg Thr Phe Gly Glu Thr Lys Met		
207	1	5	10
			15
210	Ser Asn Ala Thr Leu Ala Ser Tyr Ile Val Arg Ile Val Arg Arg Tyr		
211	20	25	30
214	Asp Ile Val Leu Ile Gln Glu Val Arg Asp Ser His Leu Val Ala Val		
215	35	40	45
218	Gly Lys Leu Leu Asp Tyr Leu Asn Gln Asp Asp Pro Asn Thr Tyr His		
219	50	55	60
222	Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr		
223	65	70	75
			80
226	226 Leu Phe Leu Phe Arg Pro Asn Lys Val Ser Val Leu Asp Thr Tyr Gln		
227	85	90	95
230	Tyr Asp Asp Gly Cys Cys Gly Asn Asp Ser Phe Ser Arg Glu Pro Ala		
231	100	105	110
234	Val Val Lys Phe Ser Ser His Ser Thr Lys Val Lys Glu Phe Ala Ile		
235	115	120	125
238	Val Ala Leu His Ser Ala Pro Ser Asp Ala Val Ala Glu Ile Asn Ser		
239	130	135	140
242	242 Leu Tyr Asp Val Tyr Leu Asp Val Gln Gln Lys Trp His Leu Asn Asp		
243	145	150	155
			160
246	246 Val Met Leu Met Gly Asp Phe Asn Ala Asp Cys Ser Tyr Val Thr Ser		
247	165	170	175
250	250 Ser Gln Trp Ser Ser Ile Arg Leu Arg Thr Ser Ser Thr Phe Gln Trp		
251	180	185	190
254	254 Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Ser Thr Asn Cys Ala		
255	195	200	205
258	258 Tyr Asp Arg Ile Val Val Ala Gly Ser Leu Leu Gln Ser Ser Val Val		
259	210	215	220
262	262 Pro Gly Ser Ala Ala Pro Phe Asp Phe Gln Ala Ala Tyr Gly Leu Ser		

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263	225	230	235	240
266		Asn Glu Met Ala Leu Ala Ile Ser Asp His Tyr Pro Val Glu Val Thr		
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270	Leu Thr			
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275	<211> LENGTH: 336			
276	<212> TYPE: PRT			
277	<213> ORGANISM: ARTIFICIAL SEQUENCE			
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284	Tyr Asp Pro Ile His Glu Tyr Val Asn His Glu Leu Arg Lys Arg Glu			
285	1	5	10	15
288	Asn Glu Phe Ser Glu His Lys Asn Val Lys Ile Phe Val Ala Ser Tyr			
289	20	25	30	
292	Asn Leu Asn Gly Cys Ser Ala Thr Thr Lys Leu Glu Asn Trp Leu Phe			
293	35	40	45	
296	Pro Glu Asn Thr Pro Leu Ala Asp Ile Tyr Val Val Gly Phe Gln Glu			
297	50	55	60	
300	Ile Val Gln Leu Thr Ser Ala Asp Pro Ala Lys Arg Arg Glu Trp Glu			
301	65	70	75	80
304	Ser Cys Val Lys Arg Leu Leu Asn Gly Lys Cys Thr Ser Gly Pro Gly			
305	85	90	95	
308	Tyr Val Gln Leu Arg Ser Gly Gln Leu Val Gly Thr Ala Leu Met Ile			
309	100	105	110	
312	Phe Cys Lys Glu Ser Cys Leu Pro Ser Ile Lys Asn Val Glu Gly Thr			
313	115	120	125	
316	Val Lys Lys Thr Gly Leu Gly Asn Lys Gly Ala Val Ala Ile Arg Phe			
317	130	135	140	
320	Asp Tyr Glu Asp Thr Gly Leu Cys Phe Ile Thr Ser His Leu Ala Ala			
321	145	150	155	160
324	Gly Tyr Thr Asn Tyr Asp Glu Arg Asp His Asp Tyr Arg Thr Ile Ala			
325	165	170	175	
328	Ser Gly Leu Arg Phe Arg Arg Gly Arg Ser Ile Phe Asn His Asp Tyr			
329	180	185	190	
332	Val Val Trp Phe Gly Asp Phe Asn Tyr Arg Ile Ser Leu Thr Tyr Glu			
333	195	200	205	
336	Glu Val Val Pro Cys Ile Ala Gln Gly Lys Leu Ser Tyr Leu Phe Glu			
337	210	215	220	
340	Tyr Asp Gln Leu Asn Lys Gln Met Leu Thr Gly Lys Val Phe Pro Phe			
341	225	230	235	240
344	Phe Ser Glu Leu Pro Ile Thr Phe Pro Pro Thr Tyr Lys Phe Asp Ile			
345	245	250	255	
348	Gly Thr Asp Ile Tyr Asp Thr Ser Asp Lys His Arg Val Pro Ala Trp			
349	260	265	270	
352	Thr Asp Arg Ile Leu Tyr Arg Gly Glu Leu Val Pro His Ser Tyr Gln			
353	275	280	285	
356	Ser Val Pro Leu Tyr Tyr Ser Asp His Arg Pro Ile Tyr Ala Thr Tyr			
357	290	295	300	

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360 Glu Ala Asn Ile Val Lys Val Asp Arg Glu Lys Lys Lys Ile Leu Phe
361 305 310 315 320
364 Glu Glu Leu Tyr Asn Gln Arg Lys Gln Glu Val Arg Asp Ala Ser Gln
365 325 330 335

VERIFICATION SUMMARY

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